Amendments to the Specification

Please replace the paragraph beginning at page 1, line 4, with the following amended paragraph (previously amended in the July 28, 2003, Preliminary Amendment):

This application is a continuation of U.S. Application No. 09/789,054, filed February 20, 2001, ~~pending~~ now abandoned, which is a continuation-in-part of U.S. Application No. 09/485,558 filed February 11, 2000, ~~pending~~ now abandoned, which was the national filing of International Application No. PCT/US98/16688 filed August 12, 1998, ~~pending~~ expired, which claims the benefit of U.S. Provisional Application No. 60/055,865, filed August 15, 1997, now abandoned.

Please replace the paragraph beginning at page 6, line 33, with the following amended paragraph:

Figure 4 shows different aspects of the yeast two-hybrid experiment designed to analyze the interaction between rice Dr1 (rDr1) and rice DRAP1 (rDRAP1) in yeast. Figure 4A is a schematic representation of the pBDGal4::rDRAP1 and pADGal4::rDr1 constructs. Gal4BD and Gal4AD indicate Gal4 DNA binding domain and Gal4 activation domain, respectively. The coding regions of rice DRAP1 and rice Dr1 were fused inframe with the coding regions for Gal4 binding domain in pBD-Gal4 Cam (Strategene, San Diego, CA) and Gal4 activation domain in pAD-Gal4-2.1 (Strategene, San Diego, CA), respectively, to produce pBDGal4::rDRAP1 and pADGal4::rDr1, respectively. The *Eco*R I and *Sma* I fragment containing the coding region of rice Dr1 was cloned into pAD-Gal4 *Eco*R I and *Sma* I sites to generate pADGal4::rDr1. The *Mfe* I and *Pst* I fragment containing the coding region of rice DRAP1 was cloned into pBD-Gal4 *Eco*R I and *Pst* I sites to generate pBDGal4::rDRAP1. Figure 4B indicates the growth of yeast transformed with different constructs in different growth media. Yeast cells were transformed with pBDGal4::rDrAp1, pADGal4::rDr1, or pBDGal4::rDrAp1 plus pADGal4::rDr1 (marked as BD, AD, and BD+AD, respectively). The yeast cells were grown on selection

media as indicated. Figure 4C summarizes the interaction of different versions of rice DRAP1 with rice Dr1. The left side is a schematic representation of the rice DRAP1 deletion mutants in pBDGal4::rDRAP1 constructs. The right side indicates the interaction of these mutants with rice Dr1. "Histone-fold" refers to histone-fold-like domain, "B" refers to basic amino acid-rich motif, "RG" stands for arginine and glycine repeat, "A1" stands for acidic amino acid-rich domain 1, "P-rich" stands for proline-rich domain, and "A2" stands for acidic amino acid-rich domain 2. "1" and "258" ~~"259"~~ indicate the amino acid residue in the encoded protein.

Please replace the paragraph beginning at page 33, line 21, with the following amended paragraph:

Sequence analysis indicated that the cDNA insert in rice clone rls12.pk0015.e12 encodes a full-length rice DRAP1 protein. The coding region in the cDNA insert is 777 bp in length and encodes a polypeptide of 258 ~~259~~ amino acids (SEQ ID NO:32) with a calculated molecular weight of 28 kDa. In the N-terminal part of the rice DRAP1 protein encoded by rice clone rls12.pk0015.e12, there is a histone fold-like structure located from residue 9 to 84 (Baxevanis and Landsman (1998) *Nucl Acids Res 26*:372-375), which has significant homology with the histone fold domain of the human DRAP1 protein (Inostroza *et al.* (1992) *Cell 70*:477-489; Goppelt *et al.* (1996) *EMBO J 15*:3105-3116; Mermelstein *et al.* (1996) *Genes Dev 10*:1033-1048), and the yeast Dr1 protein (Kim *et al.* (1997) *Proc Natl Acad Sci USA 94*:820-825). Compared with human DRAP1, there are three extra amino acid stretches in rice DRAP1 described herein. The first one is residues 94 through 113, which contains a nuclear localization signal. The second one is residues 124 through 143, which includes arginine (R) and glycine (G) repeats (RG repeat). Some transcription factors have the RG repeat domain, whose function has not been elucidated yet. The third one is residues 213 through 226, 5 of which are acidic amino acids. In the rice DRAP1 described herein (SEQ ID NO:32), there are two acidic amino acid-rich domains (residues 155 through 189 and residues 249 through 258 ~~259~~) and one proline-rich domain (residues 192 through 238). The acidic amino

acid-rich domains and proline-rich domain are often involved in activation or repression of transcription factors.

Please replace the paragraph beginning at page 40, line 30, with the following amended paragraph (please note that the underlining of the six nucleotide EcoRV restriction site, "GATATC", in each of SEQ ID NOs: 61-63 was present in the original text and does not represent a current amendment):

Using p35S::Gal4/rDRAP1 as template and oligonucleotides Q156 (SEQ ID NO:61), Q157 (SEQ ID NO:62) and Q172 (SEQ ID NO:63) as primers, an EcoRV site was introduced by site-directed mutagenesis into p35S::Gal4/rDRAP1 to produce p35S::Gal4/rDRAP1-EV3, p35S::Gal4/rDRAP1-EV4, and p35S::Gal4/rDRAP1-EV6, respectively.

Q156: 5'-AGAGGGCGAGGACGAGATATCCCACCCACCAAGCGGA-3'
(SEQ ID NO:61)
Q157: 5'-GAATCTCGATCAAGCGATATCAAAATGGCCGTAAGAA-3'
(SEQ ID NO:62)
Q172: 5'-TGTGTGAGGAGGTACGATATCAGTTCTTTTGACTTC-3'
(SEQ ID NO:63)

Plasmids p35S::Gal4/rDRAP1-EV3, p35S::Gal4/rDRAP1-EV4, and p35S::Gal4/rDRAP1-EV6 were digested with EcoRV/MscI, and then self ligated to produce p35S::Gal4/rDRAP1R148, p35S::Gal4/rDRAP1S123, and p35S::Gal4/rDRAP1Y75, respectively. p35S::Gal4/rDRAP1R148, p35S::Gal4/rDRAP1S123, and p35S::Gal4/rDRAP1Y75 encode Gal4 DNA-binding domain/rDRAP1 fusion proteins in which the rice DRAP1 protein part is truncated, lacking the C-terminal 111 amino acids, 136 amino acids, and 184 ~~166~~ amino acids, respectively, of rice DRAP1 as set forth in SEQ ID NO:32.

Please replace the paragraph beginning at page 41, line 12, with the following amended paragraph:

The results (Figure 6B) showed that deletion of the N-terminal 63 amino acids of rice DRAP1 eliminated DRAP1 repression activity. Deletion of DRAP1 C-terminal 111 amino acids gave stronger repression activity than that of the full length protein. Deletion of DRAP1 C-terminal 136 amino acids still had full repression activity, but deletion of C-terminal 184 ~~166~~ amino acids eliminated its repression activity (Fig. 6B). These results demonstrate that the N-terminal 122 ~~123~~ amino acids are sufficient for rice DRAP1 repression activity, the 48 ~~33~~ amino acids between 74 ~~93~~ and 123 are necessary for the repression activity, and the amino acids between 122 ~~123~~ and 148 are also involved in mediating strong repression activity of DRAP1.